BIS46216 603188602 BI463670 603207340 BI463670 603207340 ALZ02756 Tetrandon AG085155 Pan trog1 BI461092 603206970 AL16665 Tetrandon H87640 yw17g11.r1 BM683941 UT.E.EJ1-BM931807 UT.E.EJ1-BM931807 UT.E.EJ1-

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Run on:

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Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810038K19:McLeod syndrome gene homolog, AK007734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected CDNAs to Drepare full-length CDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AK007734.1 GI:12841469
HTC; CAP trapper.
Mus musculus (strain:C57BL/6J) 10 day old male pancreas cDNA to mRNA, clone lib:RIKEN full-length enriched mouse cDNA library clone:1810038K19.

Was musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Meth. Enzymol. 303, 19-44 (1999)
99279253
                                                                                                                                                                            CNS032YG
AQ087397
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                                                                                                            H87640
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BM931807
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BM472443
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DEFINITION
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AUTHORS
TITLE
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MEDLINE
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BC027097 Mus muscu
BE200527 BE200527
BG675952 602622310
ALG52777 ALG52777
BE031611 130228 MA
                                                                       March 30, 2003, 02:51:12 ; Search time 1672.99 Seconds (without alignments) 13446.329 Million cell updates/sec
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         GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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Maximum Match 100%
Listing first 45 summaries
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294.6
259.4
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240.6
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Maximum DB
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Database

Result

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BM470447 AGENCOURT BM466219 AGENCOURT BI463669 603207339

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ITKKRQMPKDGLSEEVEKEVGQAEGKLITHRSAFSRASVIQAFLGSAPQLTLQLYITV
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RCACWSSLRRKSSEPVGRIDTDLKACTEQDVMPTTSKVIPEATDIWTAVDLCSA"
         was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 TCCACCTTTTTGTACTGTGGGAGGCTGCATCTGCTTTGTACATGGTTAGAATCTATCGA 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414 CTGCTCATGCACCTGCTCCAGCTCGGGCCCCTGTACAGGTGTTGTGAAGTCTTTTGTATC 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cgacadaricccaaaadaricccrrrcadaccacciccadaaaadaccricccacccaccagaa 584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="McLeod syndrome gene homolog
data source:MGD, source key:MGI:103569, evidence:ISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 6.7e-72;
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                                                                cocation/Qualifiers
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/Lint. at: http://image.llnl.gov Series: IRAK Plate: 45 Row: d Column: 3 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 12963702 This clone has the following problem: frame shifted.
                                                                                                                                                             Contact: amg@bcm.tmc.edu
donaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.
Richards, S., Gibbs, R.A.
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                         cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
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ive 0; Mismatches 489; Indels
cDNA Library Preparation: Life Technologies, Inc
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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1774 bp mRNA linear HTC 07-AUG-2002 Mus musculus, McLeod syndrome gene homolog, clone IMAGE:5012421,
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 1774)
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Submitted (04-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATGCCGGCATCAACATGTTCTGCTGGTCAGCTGTTCAGCTGAAAATCGACAATCCGGAG 1124
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|GTGCGCCTCTGTTGATCTTGCAGCTGCTTATTGGGTACTGCACTGGCATTCTCTTCATG 1304
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                      GGCTCAGTGCCCCAGCTGACCTATCAGCTCTATGTGAGCCTGATCTCTGCAGAGGTTCCC
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,

Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda

M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,

Okazaki, Y., Okido, T., Saito, R., Sakai, K., Sano, H., Sasaki

D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,

Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,

Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTS (Arakawa, T., et al. 2001)

On Jun 30, 2000 this sequence version replaced gi:8865480.
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Tel: 81-45-503-9222
Pax: 81-45-503-9216
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
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The Institute of Physical and Chemical Research (RIKEN)
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Computer-based methods for the mouse full-length cDNA computer-based methods for the mouse full-length cDNA construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, Y., Itoh, M., Kawai, J., Shinagawa, A., Aizawa Ishi, Y. and Hayashizaki, Y. Mayaing of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Marsuura
Hayashizaki,Y.
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    .624
    /organism="Mus musculus"
    /db xref="taxon:10090"
    /clone="A430025D09"
    /clone=lib="RIKEN full-length enriched, 0 day neonate thymus"

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Pred. No. 5.4e-60;
0; Mismatches 16
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/dev_stage="0 day neonate"
/lab_host="DH108"
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Local Similarity 94.4%;
nes 269; Conservative
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                                                                                            RESULT 5
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| /organism="Homo sapiens" | /organism="Homo sapiens" | /organism="Homo sapiens" | /organism="Homo sapiens" | /olone="IbmAGE:4747323" | /clone="Ibm="NCI_CGAP_SKn4" | /tisk="Experism="State_1" | /lab_host="DHIOB (IT) phage-resistant) | /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not!; Site_2: Sali, Cloned unidirectionally. Primer: Oligo dT. Salee_2: Sali, Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.Skb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library." | 14 a 178 c 169 g 249 t
                                                                                                                                                                                                                         BG675952
602622310P1 NCI_CGAP_Skn4 Homo sapiens CDNA clone IMAGE:4747323 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Londott: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CONTAIN Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CLone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
LlAMIOS97 row: c column: 04
High quality sequence start: 4
High quality sequence start: 4
High quality sequence stop: 797.
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 810)
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                                544 AAACGTATGTCACAGATCCAAGCCTTCCTGGGCTCAGTGCCCCAGCTGACCTATCAGCTC 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CTTGCAGCTCATTATTGCTTATCTGATTTCCATTGGCTTCATGCTCCTTTTCTTCCAGTA 120
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Best Local Similarity 99.6%; Pred. No. 1.5e-56;
Matches 258; Conservative 0; Mismatches 0; Indels
                                                                                      TATGTGAGCCTGATCTCTGCAGAGGTTCCCCTGGGTAGAGTTGTG 648
                                                                                                              BG675952.1, GI:13907348
                                                                                                                                                                                                                                                             mRNA sequence.
BG675952
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                                                                                                                                                                                                                                                                                                                                              human.
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BG675952
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DEFINITION
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Email: trop@sanger.ac.uk
Sanger Xenpous tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TGas029g15.sp6
Sequencing primer: $F6
This sequence is from a Xenopus Gene Collection (XGC) library
Constructed by Aaron M. Zorn.

1. 676
Ab zreq="taxon:sla"
Ab zref="taxon:sla"
Ab zref="taxon:sla"
Ab zref="taxon:sla"
Aclone="TGas029g15"
Aclone="taxon:sla"
Aclone="taxon:sla"
Alab—host="Bacherichia coli XL1-blue"
Anote="Vaccqastrula"
Anote="vaccqrs"
Anotes" astrula (stages 10.5-13 mixed)"
Anotes" vaccor: pCS107; Site 1: EcoRI; Site 2: NotI; CDNA was oligo dT primed from 5ug of poly A+ RNĀ from stages
10-13 gastrulae.
EcoRI.obcl cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3'
                                                                                                                                                                                                                                              AL652777 AL652777 XGC-gastrula Silurana tropicalis cDNA clone TGas029915 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Silurana tropicalis
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACTICAGCCGGGTCGGCACTCTGGTGGTCCTGATTTCAGTCACCATCCTCTATGCTGGC 1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               703 TIGGCTATCCAGATCAAGTACGATGACTACAAGATTCGCCCTTGGGCCACTAGAAGTCCTC 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCATCACCATCTGGCGGACATTGGAGATCACTTCCCGCCTCCTGATTCTGGTGCTCTTC 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 rechricareareredeagarereredagarrechacecererracagricagererrir 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.

Sanger Xenopus tropicalis EST project 2001 (10_2001)

Unpublished (2001)
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Pred. No. 8.1e-55;
0; Mismatches 269; Indels 0
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1371 AAGGCAAAGTGTTGTCTGA 1389
                                                                    240 AAGGCAAAGTGTTGTCTGA 258
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Best Local Similarity 59.9%;
Matches 402; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                     western clawed frog
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Sanger Centre
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26; Indels

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1230 CATGCTCCTTTTCTTCCAGTACTTGCATCCATTGCGCTCACTCTTCACCCATAATGTAGT 1289
                                                                                                                                                                                                                                                                                                                                                                       1290 AGACTACCTCCATTGTGTCTGCTGTCACCAGCACCCTCGGACCAGGGTTGAGAACTCAGA 1349
                                                                           1110 GGTAGAGAATGTGATCATGGTCTTGGTTTTTAAGTTCTTTGGAGTGAAAGTGTTACTGAA 1169
                                                                                                                                                                         1170 TTACTGTCATTCCTTGATTGCCTTGCAGCTCATTATTGCTTATCTGATTTCCATTGGCTT 1229
                                                                                                                                                                                                                                                                                                                                                                                                                  182 geachaceraciererereciecarcaeacacereceseseses 241
                                                                                                       2 GGTAGAGAACGTGATCATGGTCTTGGTTTTTAAGTTCTTTGGAGTGAAAGTGTACTGGA
                                                                                                                                                                                                     THACTGTCATTCCTCGATTGCTTTGCAGCTCATTATTGCTTACCTGATTTCCATTGGCTT
                                                                                                                                                                                                                                                                                                     122 CATGCTCCTTTTCTTCCAGTACTTGCACCCGCTGCGCTCACTTCTCACCCACAACGTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCACCCTTTGAGACTGAAGCAAGGCAAAGTGTTGTCTGA 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 gecarcrerrangergergaacaagecagagearrerga 281
  Pred. No. 2.6e-54;
                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence. _ _ BI827782
BI827782
BI827782.1 GI:15939332
90.78;
                              Matches 254; Conservative
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     Best Local Similarity
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ORIGIN
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TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
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KEYWORDS
SOURCE
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BI827782
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 09-JUL-2000
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1 (bases 1 to 392)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000) Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /notē="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from day 11, 13, 15, 20,
                                                                                                                                                                                                                                                1123 ATCATGGTCTTGGTTTTTAAGTTCTTTGGAGTGAAAGTGTTACTGAATTACTGTCATTCC 1182
                                                                                                                                                                                                                                                                                                                                                1183 TTGATTGCCTTGCAGCTCATTATTGCTTATCTGATTTCCATTGGCTTCATGCTCCTTTTC 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                1243 TTCCAGTACTTGCATCCATTGCGCTCACTCTTCACCCATAATGTAGTAGACTACCTCCAT 1302
                                                                                                                                                  .063 AAAGGGCAGAACTGGGGACATATGGGCCTGCACTATAGTGTGAGGTTGGTAGAGAATGTG 1122
                                                                                                                                                                                                                                                                                                                                                                            546 CTGCTGGTGGTTCAACTCTTAGTAGAATATGCCACCGCCATCTTCTTCATGCTTTTTT 605
  306 AACTTTAGCTGGTTTGGTACTGTGACAGTCCTTGGGTCAGTAACCTTGCTTTATTCAGCC 365
                                                                                                  366 ATCAATATGTTTTGCTGGTCTGCTGTTCAGCTAAACCTATCAGATCGGGACTTAATTGAC 425
                                                                                                                                                                                                426 CAGTCACAAAACTGGGGGAGGTTAAGTCTTTATACCATTCGGTTGCTCGAGAATGCA 485
                                                                                                                                                                                                                                                                                                486 GCCCTCATTCTGCTCTGGTACTTCTACAAGGAGGATGTGTTTGAGTATTTCTGTTCCCCA 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              606 raccadraccrrcacccrraccedrraccrrrrcacceacaacerraadacrerracer 665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE031611 392 bp mRNA linear 130228 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BACKWARD: GTTTTCCCAGTCACGACG
Plate: 59 row. c column: 17
Seg primer: ATTAAGGTGACACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       embryos."
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Sus
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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BE031611
LOCUS
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BI827782 881 bp mRNA linear EST 04-OCT-2001
603075458F1 NIH_MGC_119 Homo sapiens CDNA clone IMAGE:5167070 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 881)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Lncyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

plate: LLAM11415 row: d column: 15

High quality sequence stop: 782.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MCC http://mgc.nci.nih.gov/.
NAH-MCC http://mgc.nci.nih.gov/.
NAtional Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 881;
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Pred. No. 2.5e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Invitrogen). Research Genethis is a NIH MGC Library."
163 c 194 g 266 t
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db_xref="taxon:9606"
clone="IMAGE:5167070"
clone lib="NIH MGC 119"
/tissue type="medulTa"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.8%;
56.8%;
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Best Local Similarity
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]. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and clonned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL638533 XGC-neurula Silurana tropicalis cDNA clone TNeu018n12 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Silurana tropicalis
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Silurana.
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 201)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP ttps://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                                                               Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1241 Std Brror: 0.00
Seg primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 183.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITAAGTICITIGGAGIGAAAGIGITACIGAATTACIG 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1176 TCATTCCTTGATTGCCTTGCACTCATTATTGCTTATCTGATTTCCATTGGCTTCATGCT 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1236 CCTTTTCTTCCAGTACTTGCATCCATTGCGCTCACTCTTCACCCATAATGTAGTAGACTA 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAATGTGATCATGGTCTTGGTTTTTAAGTTCTATGGAGTGAAGTGTTACTGAATTACTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        constructed by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TCATTCCTTGATTGCCTTGCACTCATTATTGCTTATCTGATTTCCATTGGCTTCATGCT
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0
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                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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                                                                                                           Tumor Gene Index
Unpublished (1997)
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AL638533
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AL638533/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
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VERSION
KEYWORDS
                                              REFERENCE
AUTHORS
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                                                                                      TITLE
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2828060:x1 NCI_CGAP_GCB1 Homo sapiens CDNA clone IMAGE:686506 5',
                                                                                                                                                                                                                                    CCATCAGCTTTATTATTGTGGGGGCAATTTTGGATCAAATTATCCTGATGTTTTTCAACA 331
                                                                                                                                                                                                       128 GATTTACTTTTCCATTTAGCATCCTTTTCTCCCACCTTTTTGTACTGTGGGGAGGCTGCAT 187
                                                                                                                                                                                                                                                                                     188 CIGCITIGIACAIGGITAGAAICTAICGAAAGAATAGIGAAACTTACTGGAIGACATACA 247
                                                                                                                                                                                                                                                                                                                               TTGGTTTATACATGTTTGAAATTTATCGAAAAGCTAATGACACATTCTGGATGTCATTTA 271
                                                                                                                                                                                                                                                                                                                                                                    CCTTTTCTTTCTTTATGTTTTCATCCATTATGGTCCAGTTGACCCTCATTTTTGTCCACA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGATCTAGCCAAAGATAAACCGCTATCATTATTATGCATCTAATCCTCTTGGGACCTG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 AAGACTIGAGGAGAAATAAGGCTGCATTACTTTTGTGGCACATTCTTCTTTTAGGACCTA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428 AGGAGCCCTATGTCAGCCTCACCCGAAAGAAGATGCTAATAGATGGCGAGGAGGTGCTGA 487
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                                                                                                                                                                                  Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE 1D: TNeu018112.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Asron M. Zorn.
Location/Qualifiers
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   Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
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RESULT 10

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S. NIH-MGC http://mgc.nci.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Trissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone discribution: MGC clone discribution information can be
http://image.llnl.gov. c column: 02
http://image.llnl.gov. c column: 02
High quality sequence stop: 707.
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/db xref="taxon:966"
/clone='InAGE:5259961"
/clone='InAGE:5259961"
/clone='InAGE:5259961"
/clone='InBell MIH MGC 95"
/tissue_type="hlppocampus"
/lab_host='BH10B"
/note='Organ: brain; Vector: pBluescriptk (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag pluescript KS+); Site_1: SalI-XhoI (gtcgag pluescript KS+); Site_1: SalI-XhoI (gtcgag pluescript KS+); Site_1: SalI-XhoI (g
603188602F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5259961 5', mRNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 793)
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In Unpublished (1999)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-romail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
Clone distribution: MGC clone distribution information can be http://image.llnl.gov
Plate: LLAM11689 row: o column: 09
High quality sequence stop: 826.
Location/Qualifiers
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603207340F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5273312 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaila; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 855)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                        945 CTICAGCCGGGICGCCACTCTGGIGGICCTGATTTCAGICACCATCCTCTAIGCTGGCAT 1004
                                                                                                                                                                                                                                                                                                                                                                                                  592 GTACCCCTGGATCCTCTTCTGGTGCAGTGGTTCCCCATTCCTGAGAACATAGAG-AAGG 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    646 GIGCTAAIGGIAITITCCCIGGIAICIGICACCIAIGGGGCCACCCTITGCAAIAIGIIG 705
                                                                                 764
                                                                                                                                                                412 GCCATCAAATCAAGTACGATGAGTATGAAGTCAAGAGTGAAGCCTCTGGCCTATGTCTG 471
                                                                                                                                                                                                             824
                                                                                                                                                                                                                                                 472 TATCTTCCTGTGGAGGAGCTTTGAGATTGCCACTCGAGTTGTAGTCCTGGTCCTCTTTAC 531
                                                                                                                                                                                                                                                                                        825 AGCCACTITGAAATIGAAGGCTGTGCCCTTCCTAGTGCTCAACTICCTGATCATCCTCTT 884
                                                                                                                                                                                                                                                                                                                                532 CTCCGTCCTGAAGACCTGGGGGGGGGTTATAATACTCATCAACTTCTTCAGTTTCTTCTA 591
                                                                                                                                                                                                                                                                                                                                                                         885 TGAGCCCTGGATTAAGTTCTGGAGAAGTGGTGCCCAGATGCCCCAATAACATTGAGAAAAA 944
292 CAGCTGACCCTACAGCTGTACATAAGTGTCATGCAGCAGGACGTCACTGTTGGAAGAAGT 351
                                                                                                                         706 GCTATCCAGATCAAGTACGATGACTAC-AAGATTCGCCTTGGGCCACTAGAAGTCCTCTG
                                                                                                                                                                                                        765 CATCACCATCTGGCGGACATTGGAGATCACTTCCCGCCTCCTGATTCTGGTGCTCTTCTC
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/db xref="taxon:9606"
/clone="ImAGE:527312"
/clone lib="WIH MGC_97"
/lab_host="DH10B"
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BI463670.1 GI:15254326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1005 CAACTTCTCTTGCTGGT 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    711 TTAACCATGTTCCTGCT 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
BI463670
LOCUS
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185 bp mRNA linear EST 09-FEB-1998 vs61c09.rl Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:1150768 5' similar to SW:XK\_HUMAN P51811 MEMBRANE TRANSPORT PROTEIN XK ;, mRNA sequence. Mus musculus

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Futheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.

( bases 1 to 385)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and ä Institutes of Health), Note: this is a NIH\_MGC Library." 156 c 186 g 256 t 187 247 537 547 311 307 367 427 491 AGGAGCCCTATGTCAGCCTCACCCGAAAGAAGATGCTAATAGATGGCGAGGAGGTGCTGA 487 597 657 Gaps CAAGGAAGCGAGAAAAATAAGCACCCTGAGAATGGAGACAGTGTTTGAAGAGAGATG 131 68 AGCCAAATGTGGATCCGGTTTCATCTCTGGAGGAAGATGTCATCCGTGGAGCCAACCCCC 127 132 AAGAAAGCACAGGAGGAGTTTCATCTTCGAAAGAAGAAATAGTCCTTGGCCAGAGACTCC 191 192 ATCTAAGCTTTCCTTTTAGCATTATCTTCTCAACTGTTCTCTACTGTGGTGAGGTTGCCT 251 ccarcagcriratratrategggggcarirriggarcaarratccrcargrirricaaca 371 372 AAGACTTGAGGAGAAATAAGGCTGCATTACTTTTTTGGCACATTCTTCTTTTAGGACCTA 431 548 GTATGTCACAGATCCAAGCCTTCCTGGGCTCAGTGCCCCAGCTGACCTATCAGCTCTATG 607 67 252 TIGGITIATACATGITIGAAATITATGGAAAAGCTAAATGACCAATGACACATTCTGGATGTCATTTA 598 ACAIGICAGIGATICAGGCTTTTCTCGGTTCTGTTCCACAATTAATTTTGCAGATGTATA 8 CAAGACCACAAAATTCAGAAAGAACCTCGACAATGGACAGAGTTTATGAAATTCCTGAGG GATITACTITICCATTIAGCATCCTTTTTCTCCCACCTTTTTGTACTGTGGGGAGGCTGCAT TTGTGAGGTGTTTGCACACATTAGAAATTACCACAAATGGTTGAAAAATCTTAAACAGG 488 TAGAATGGGAGGTGGGCCACTCCGATCCGGACCTGGCTATGCACGCAATGCCTACAAAC CTGCTTTGTACATGGTTAGAATCTATCGAAAGAATAGTGAAACTTACTGGATGACATACA CCTTTTCTTTCTTTATGTTTTCATCCATTATGGTCCAGTTGACCCTCATTTTTGTCCACA GAGATCTAGCCAAAGATAAACCGCTATCATTATTTATGCATCTAATCCTCTTGGGACCTG TTATCAGATGTTTGGAGGCCATGATTAAGTACCTCACACTGTGGAAGAAGAGGAGGAGG AGAAGGAAGA-------GACTCAAGTTAGCATCACAAAGAAAACACGATGCT 538 GGCAAAGGGAGATTGCATTCTCAATCCGGGATAATTTCATGCAGCAGAAGGCTTTCAAGT 14; DB 13; Length 855; Score 174.2; DB 13; Length Pred. No. 1.5e-36; 0; Mismatches 248; Indels

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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                          Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
Unpublished
                                                                                                                                2 (bases 1 to 691)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,

Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and

Weissenbach, J.

Charaterization and repeat analysis of the compact genome of the

freelwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="G"
/note="Genoscope sequence ID : COAG147BE08LP1~end : T7"
182 c 187 g 189 t 5 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTGATCATCCTCTTTGAGCCCTGGATTAAGTTCTGGAGAAGTGGTGCCCAGATGCCCA 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      377 TGCTCTTCTTCTTCCAACCCTGGACCGAGTTCTGGGCCAAGAAAGGCTCGTTGACTC 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 929 ATAACATTGAGAAAAACTTCAGCCGGGTCGGCACTCTGGTGGTCCTGATTTCAGTCACCA 988
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Pred. No. 1.5e-35;
2; Mismatches 210; Indels
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/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="147116"
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            Saurin, W. and Weissenbach, J.
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Submitted (12-APR-2000)
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58.9%;
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Best Local Similarity 58.9
Matches 305; Conservative
                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                                                             gh LLNL ; contact the
further information.
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The WashU-HHMI Mouse EST Project Unpublished (1996)
Contact: Marra MyNouse EST Project WashU-HHMI Mouse EST Project WashIngton University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Pax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 173.2; DB 9; Length 385; Pred. No. 2.1e-36; 0; Mismatches 13; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rolone="IMAGE:1150768"
/clone_lib="Stratagene mouse skin (#937313)"
                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through
IMAGE Consortium (info@image.llnl.gov) for fu
MGIS1623976
                                                                                                                                                                                                                                                                                                                                                             Seg primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 378.
Location/Qualifiers
1. .385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="whole skin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL202756.1 GI:7861101
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sex="Females"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
12.5%;
Best Local Similarity 93.3%;
Matches 181; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGGTAGAGTTGTG 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ø
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CNS02LFV
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REPERENCE AUTHORS

TITLE JOURNAL REFERENCE AUTHORS

TITLE

COMMENT

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BI461092 666 bp mRNA linear EST 21-AUG-2001
603206970F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5272840 5',
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 666)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Miklos J. Brownstein (NHGRI), Shiral
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1688 row: k column: 17
High quality sequence stop: 663.
High quality sequence stop: 663.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 ATGGTCCAGTTGACCCTCATTTTTGTCCACAGAGATCTAGCCAAAGATAAACCGCTATCA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       276 chośneckachokachornomyckockakonowachokackockachokaka 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   337 TTATTTATGCATCTAATCCTCTTGGGACCTGTTATCAGATGTTTGGAGGCCATGATTAAG 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 CTGCTGCTGCACCTGCTGCACTTGGGCCCCTTTTCAGGTGTTTTGAAGTCTTCTGCATC 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             397 TACCTCACACTGTGGAAGAAGAGAGCAGGAGGAGCCCTATGTCAGCCTCACCCGAAAG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    396 TACTTTC-----AGTCAGGCAACAATGAAGAGCCTTATGTCAGTATCACCAAGAAG 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          457 A---AGATGCTAATAGATGGCGAGGAGGTGCTGATAGAATGGGAGGTGGGCCACTCCATC 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH WCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 TCCACCTTTTTGTACTGTGGGGGGCTGCATCTGCTTTGTACATGGTTAGAATCTATCGA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.9%; Score 109.2; DB 13; Length 666; 53.7%; Pred. No. 9.5e-19; ive 0; Mismatches 228; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 666
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="TWAGE:5272840"
/clone=lib="NIH MGC_97"
/lab_host="DH10B"
                                                                                      mRNA sequence. ____B1461092
B1461092.1 GI:15251748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                               Homo sapiens
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Matches 278;
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                                                                                                                                                                                                                                                                                                                                                                                                              Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submitseion
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbesegger.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tlei:81-45-503-9111, Fax:81-45-503-9170,
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                          Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-083B22.F.
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
Pan troglodytes DNA, clone: PTB-083B22.F, genomic survey sequence
                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         640 AGAGTIGIGCIAATGGIATTITCCCTGGIATCTGTCACCTATGGGGCCACCCTTTGCAAT 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   700 ATGTTGGCTATCCAGATCAAGTACGATGACTACAAGATTCGCCTTGGGCCACTAGAAGTC 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294 ATACTGGCCATCCAGATCAGCAATGATGATACTACCACTAAGCTACCGCCGATAGAATTC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCTGCATCACCATCTGGCGGACATTGGAGATCACTTCCCGCCTCCTGATTCTGGTGCTC 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 TTCTGTGTGGTGATGTGGCGTTTTTTGGAGGTTATCTCACGTGTAGTGACTCTGGCATTT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TICTCAGCCACTITGAAATIGAAGGCTGTGCCCTTCCTAGTGCTCAACTTCCTGATCATC 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354 ATAGCATIGCIGAIGACAIGITCCCIGITATCAGITACTIAIGGGGCCATICGCIGCAAI 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          880 CTCTTTGAGCCCTGGATTAAGTTCTGGAGAAGTGGTGCCCAGATGCCCAATAACATTGAG
                                                                                                                                                                                                                                                                                Taylor, T.D., Yada, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
151 c 127 g 181 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
8.1%; Score 113.2; DB 17; Length
Best Local Similarity 60.9%; Pred. No. 7.7e-20;
Matches 184; Conservative 0; Mismatches 118; Indels
                                                                                                                                                                                                                                                                          Fujiyama,A., Hattori,M., Toyoda,A., 1
TotoKi,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .691
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-083B22.F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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R.Site 2 : Saci
                                                      AG085155.1 GI:16636957
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                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 691)
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FEATURES

BASE COUNT ORIGIN

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